



SEQUENCE LISTING

<110> Johnson, Leslie S.

Li, Hua

Tuailon, Nadine

<120> SOLUBLE FCgammaR FUSION PROTEINS AND METHODS OF USE THEREOF

<130> 11183-005-999

<140> 10/756,153

<141> 2004-01-13

<150> 60/439,709

<151> 2003-01-13

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<170> FastSEQ version 4.0

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<211> 420

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIa-G2

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Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
35 40 45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
50 55 60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
65 70 75 80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala
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Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His

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Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Asn	Ile	Thr	Ile	Thr	Gln	Gly
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Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val
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Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
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				245					250					255	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr
			260					265					270		
Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn
		275					280					285			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro
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Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
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		355					360					365			
Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
	370					375					380				
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
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<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIb-G2

<400> 2

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Thr	Leu	Phe	Ser	Ser	Lys	Pro	Val	Thr	Ile	Thr	Val	Gln	Ala	Pro	Ser
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Ser	Ser	Pro	Met	Glu	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys
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Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
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Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr
225					230					235					240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 245 250 255
 Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
 260 265 270
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 275 280 285
 Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
 290 295 300
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 305 310 315 320
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 325 330 335
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 340 345 350
 Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 355 360 365
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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 Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 3

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIa(131R)-G2

<400> 3

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 20 25 30
 Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
 35 40 45
 His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
 50 55 60

Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	Pro	Val	His	65	70	75	80
Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	His	Leu	Glu		85	90	95
Phe	Gln	Glu	Gly	Glu	Thr	Ile	Met	Leu	Arg	Cys	His	Ser	Trp	Lys	Asp	100	105	110	
Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	Ser	Gln	Lys	115	120	125	
Phe	Ser	Arg	Leu	Asp	Pro	Thr	Phe	Ser	Ile	Pro	Gln	Ala	Asn	His	Ser	130	135	140	
His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr	Thr	Leu	Phe	145	150	155	160
Ser	Ser	Lys	Pro	Val	Thr	Ile	Thr	Val	Gln	Val	Pro	Ser	Met	Gly	Ser	165	170	175	
Ser	Ser	Pro	Met	Glu	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	180	185	190	
Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	195	200	205	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	210	215	220	
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	225	230	235	240
Val	Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	245	250	255	
Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	260	265	270	
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	275	280	285	
Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	290	295	300	
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	305	310	315	320
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	325	330	335	
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	340	345	350	
Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	355	360	365	
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	370	375	380	
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln				

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 Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
 20 25 30
 Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
 35 40 45
 His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
 50 55 60
 Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
 65 70 75 80
 Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
 85 90 95
 Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
 100 105 110
 Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
 115 120 125
 Phe Ser His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
 130 135 140
 His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
 145 150 155 160
 Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser
 165 170 175
 Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
 180 185 190
 Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 195 200 205
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

210	215	220
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr		
225	230	235 240
Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu		
	245	250 255
Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His		
	260	265 270
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys		
	275	280 285
Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln		
	290	295 300
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met		
305	310	315 320
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro		
	325	330 335
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn		
	340	345 350
Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu		
	355	360 365
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val		
	370	375 380
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln		
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Lys Ser Leu Ser Leu Ser Pro Gly Lys		
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<212> DNA

<213> Homo sapiens

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<223> sFcRIIB insert with signal sequence

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ggctcctgtt gctgggacac ctgcagctcc cccaaaggct gtgctgaaac tcgagcccca	180
gtggatcaac gtgctccagg aggactctgt gactctgaca tgccggggga ctcacagccc	240

tgagagcgac tccattcagt ggttccacaa tgggaatctc attcccaccc acacgcagcc	300
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gaccagcctc agcgaccctg tgcattctgac tgtgctttct gagtggctgg tgctccagac	420
ccctcacctg gagttccagg agggagaaac catcgtgctg aggtgccaca gctggaagga	480
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cagctcttca cccatggagg agcgcaaatg ttgtgtcgag tgcccaccgt gcccagcacc	720
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cacacctccc atgctggact ccgacggctc cttcttctc tacagcaagc tcaccgtgga	1260
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<213> Homo sapiens

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ctccacaggt gtccactcca tgcggactga agatctcccc aaggctgtgg tgttcctgga	180
gcctcaatgg tacaggggtgc tcgagaagga cagtgtgact ctgaagtgcc agggagccta	240
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<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIA-131H

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<212> DNA

<213> Homo sapiens

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<223> sFcRIIA-131R

<400> 8

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ggctcctggt gctgggacac ctgcagctcc cccaaaggct gtgctgaaac ttgagccccc      180
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cctgccccca tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa     1140
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<213> Homo sapiens

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<223> human FcRIIa

<400> 9

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20 25 30
Ser Gln Ala Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro
35 40 45
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65 70 75 80
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Asn Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser
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Pro His Leu Glu Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His
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<212> PRT

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<223> Membrane proximal domain of RIIb

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tgagtggcat gagggaggca gagtgggtc	2009

<210> 32

<211> 326

<212> PRT

<213> Homo sapiens

<220>

<223> Human IgG2

<400> 32

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Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	
			20					25					30			
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
		35					40					45				
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	
	50					55						60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	
65					70					75					80	
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	
			85						90					95		
Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
			100					105					110			
Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
			115					120					125			
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
	130					135					140					
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
145					150					155					160	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	
				165					170					175		
Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	
			180					185					190			
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	
		195					200					205				
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	
	210					215					220					
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	
225					230					235					240	
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	

	245		250		255										
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr
		260						265					270		
Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys
		275					280					285			
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys
	290					295					300				
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
305					310					315					320
Ser	Leu	Ser	Pro	Gly	Lys										
				325											

<210> 33

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V1

<400> 33

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acacagtggg ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180
gctgccacag tcgacgacag tggagagtac aggtgccaga caaacctctc caccctcagt 240
gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300
ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360
aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatacataa ttctgacttc 420
tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttggtggg 480
agtaaaaatg tgtcttcaga gactgtgaac atcaccatca ctcaagggtg cgaggatca 540
gagcgcaaat gttgtgtcga gtgccaccg tgccagcac cacctgtggc aggaccgtca 600
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 660
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gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 780
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aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 960
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 gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacacctcc catgctggac 1080
 tccgacggct ccttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1140
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<210> 34

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V1

<400> 34

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Trp	Tyr	Arg	Val	Leu	Glu	Lys	Asp	Ser	Val	Thr	Leu	Lys	Cys	Gln	Gly	20	25	30	
Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu	Ser	35	40	45	
Leu	Ile	Ser	Ser	Gln	Ala	Ser	Ser	Tyr	Phe	Ile	Asp	Ala	Ala	Thr	Val	50	55	60	
Asp	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Thr	Asn	Leu	Ser	Thr	Leu	Ser	65	70	75	80
Asp	Pro	Val	Gln	Leu	Glu	Val	His	Ile	Gly	Trp	Leu	Leu	Leu	Gln	Ala	85	90	95	
Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys	His	100	105	110	
Ser	Trp	Lys	Asn	Thr	Ala	Leu	His	Lys	Val	Thr	Tyr	Leu	Gln	Asn	Gly	115	120	125	
Lys	Gly	Arg	Lys	Tyr	Phe	His	His	Asn	Ser	Asp	Phe	Tyr	Ile	Pro	Lys	130	135	140	
Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Val	Gly	145	150	155	160
Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Asn	Ile	Thr	Ile	Thr	Gln	Gly	165	170	175	

Gly	Gly	Gly	Ser	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro			
			180					185					190					
Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro			
		195					200					205						
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val			
	210					215						220						
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val			
225					230					235					240			
Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln			
				245					250					255				
Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln			
			260					265						270				
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly			
	275						280					285						
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro			
	290					295					300							
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr			
305					310					315					320			
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser			
				325					330					335				
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr			
		340						345					350					
Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr			
		355					360					365						
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe			
	370					375					380							
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys			
385					390					395					400			
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys											
				405														

<210> 35

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

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acacagtggg ttacacaatga gagcctcatt tcaagccagg cctcgagcta cttcattgac 180
gctgccacag tgcacgacag tggagagtag aggtgccaga caaacctctc caccctcagt 240
gacccgggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcgggtgggtg 300
ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360
aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatacataa ttctgacttc 420
tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggtg 480
agtaaaaatg tgtcttcaga gactgtgacc atcaccatca ctcaagggtg cggaggatca 540
gagcgcaaat gttgtgtcga gtgcccaccg tgcccagcac cacctgtggc aggaccgtca 600
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acgtgcgtgg tgggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg 720
gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 780
ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtac 840
aagtgcagg tctccaacaa aggctccca gccccatcg agaaaaccat ctccaaaacc 900
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 960
aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct accccagcga catcgccgtg 1020
gagtgggaga gcaatgggca gccggagaa aactacaaga ccacacctcc catgctggac 1080
tccgacggct ccttcttct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1140
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<210> 36

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

<400> 36

Met	Arg	Thr	Glu	Asp	Leu	Pro	Lys	Ala	Val	Val	Phe	Leu	Glu	Pro	Gln
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Trp	Tyr	Arg	Val	Leu	Glu	Lys	Asp	Ser	Val	Thr	Leu	Lys	Cys	Gln	Gly			
			20					25					30					
Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu	Ser			
		35					40					45						
Leu	Ile	Ser	Ser	Gln	Ala	Ser	Ser	Tyr	Phe	Ile	Asp	Ala	Ala	Thr	Val			
	50					55					60							
Asp	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Thr	Asn	Leu	Ser	Thr	Leu	Ser			
65					70					75					80			
Asp	Pro	Val	Gln	Leu	Glu	Val	His	Ile	Gly	Trp	Leu	Leu	Leu	Gln	Ala			
			85						90					95				
Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys	His			
			100					105					110					
Ser	Trp	Lys	Asn	Thr	Ala	Leu	His	Lys	Val	Thr	Tyr	Leu	Gln	Asn	Gly			
		115					120					125						
Lys	Gly	Arg	Lys	Tyr	Phe	His	His	Asn	Ser	Asp	Phe	Tyr	Ile	Pro	Lys			
	130					135					140							
Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Val	Gly			
145					150					155					160			
Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Thr	Ile	Thr	Ile	Thr	Gln	Gly			
			165						170					175				
Gly	Gly	Gly	Ser	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro			
			180					185					190					
Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro			
		195					200					205						
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val			
	210					215					220							
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val			
225					230					235					240			
Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln			
			245						250					255				
Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln			
			260					265					270					
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly			
		275					280					285						
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro			
	290					295					300							
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr			
305					310					315					320			
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser			
			325						330					335				

Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
			340					345					350		
Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			355				360					365			
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
	370					375					380				
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
385					390					395					400
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
				405											

<210> 37

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V3

<400> 37

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acacagtggg ttcaaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180
gctgccacag tgcagcacag tggagagtac aggtgccaga caaacctctc caccctcagt 240
gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300
ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360
aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420
tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggg 480
agtaaaaatg tgtcttcaga gactgtgaac atcactgtcc aagctcccag ctcttcaccc 540
atggaggagc gcaaagtgtg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga 600
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctc 660
gaggtcacgt gcgtgggtgg ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg 720
tacgtggacg gcatggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac 780
agcacgttcc gtgtggtcag cgtcctcacc gtcgtgcacc aggactggct gaacggcaag 840
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aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 960
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gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1080
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1140
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1200
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<210> 38

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V3

<400> 38

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      20              25              30
Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
      35              40              45
Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
      50              55              60
Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
      65              70              75              80
Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala
      85              90              95
Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His
      100             105             110
Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly
      115             120             125
Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys
      130             135             140
Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly
      145             150             155             160
Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Val Gln Ala Pro
      165             170             175

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Ser	Ser	Ser	Pro	Met	Glu	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro		
			180					185					190				
Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro		
		195					200					205					
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys		
	210					215					220						
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp		
	225				230					235					240		
Tyr	Val	Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu		
				245					250					255			
Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val		
			260					265					270				
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn		
		275					280					285					
Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly		
	290					295					300						
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu		
	305				310					315					320		
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr		
				325					330					335			
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn		
			340					345					350				
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe		
		355					360					365					
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn		
	370					375					380						
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr		
	385				390					395					400		
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
				405					410								

<210> 39

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V4

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 acacagtggg ttccacaatga gagcctcatt tcaagccagg cctcgagcta cttcattgac 180
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 gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcgggtgggtg 300
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 aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatacataa ttctgacttc 420
 tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttggtggg 480
 agtaaaaatg tgtcttcaga gactgtgacc atcactgtcc aagctcccag ctcttcaccc 540
 atggaggagc gcaaagtgtg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga 600
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctc 660
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<212> PRT

<213> Homo sapiens

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<223> sFcRIIAG2-V4

<400> 40

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Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu	Ser	
		35					40					45				
Leu	Ile	Ser	Ser	Gln	Ala	Ser	Ser	Tyr	Phe	Ile	Asp	Ala	Ala	Thr	Val	
	50					55					60					
Asp	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Thr	Asn	Leu	Ser	Thr	Leu	Ser	
65					70					75					80	
Asp	Pro	Val	Gln	Leu	Glu	Val	His	Ile	Gly	Trp	Leu	Leu	Leu	Gln	Ala	
			85						90					95		
Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys	His	
			100					105					110			
Ser	Trp	Lys	Asn	Thr	Ala	Leu	His	Lys	Val	Thr	Tyr	Leu	Gln	Asn	Gly	
		115					120					125				
Lys	Gly	Arg	Lys	Tyr	Phe	His	His	Asn	Ser	Asp	Phe	Tyr	Ile	Pro	Lys	
	130					135					140					
Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Val	Gly	
145					150					155					160	
Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Thr	Ile	Thr	Val	Gln	Ala	Pro	
			165						170					175		
Ser	Ser	Ser	Pro	Met	Glu	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	
			180					185					190			
Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
		195					200					205				
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
	210					215					220					
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	
225					230					235					240	
Tyr	Val	Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
			245						250					255		
Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	
			260					265					270			
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
		275					280					285				
Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	
	290					295					300					
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	
305					310					315					320	

Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			325						330					335	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
			340					345					350		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		355					360					365			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
	370					375					380				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
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Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
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<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIBG2-N297Q

<400> 41

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gtcacgtgcg tgggtgtgga cgtgagccac gaagaccccg aggtccagtt caactggtac 720
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<400> 42

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		20						25					30		
His	Ser	Pro	Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu
		35					40					45			
Ile	Pro	Thr	His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn
	50					55					60				
Asp	Ser	Gly	Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp
65					70					75				80	
Pro	Val	His	Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro
			85						90					95	
His	Leu	Glu	Phe	Gln	Glu	Gly	Glu	Thr	Ile	Val	Leu	Arg	Cys	His	Ser
		100						105					110		
Trp	Lys	Asp	Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys
		115					120					125			
Ser	Lys	Lys	Phe	Ser	Arg	Ser	Asp	Pro	Asn	Phe	Ser	Ile	Pro	Gln	Ala
	130					135					140				
Asn	His	Ser	His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr
145					150					155				160	

Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser
 165 170 175
 Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
 180 185 190
 Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 195 200 205
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 210 215 220
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
 225 230 235 240
 Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 245 250 255
 Gln Phe Gln Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
 260 265 270
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 275 280 285
 Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
 290 295 300
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 305 310 315 320
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 325 330 335
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 340 345 350
 Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 355 360 365
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaRIIIA F/G loop region fragment

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<213> Artificial Sequence

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<223> FcgammaRIIIIA F/G loop region mutant

<400> 44

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1 5

<210> 45

<211> 16

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaRIIIIA-G2 extracellular domain C-terminal fragment

<400> 45
Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln Val
1 5 10 15

<210> 46

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> flexible linker sequence

<400> 46
Gly Gly Gly Gly Ser
1 5

<210> 47

<211> 20

<212> PRT
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 <223> FcgammaRIIIA-G2 extracellular domain C-terminal fragment
 <400> 47
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 1 5 10 15
 Gly Tyr Gln Val
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<210> 48
 <211> 10
 <212> PRT
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 <400> 48
 Val Gln Ala Pro Ser Ser Ser Pro Met Glu
 1 5 10

<210> 49
 <211> 24
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 <223> FcgammaRIIIA-G2 wild type subsequence
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 Phe Phe Pro Pro Gly Tyr Gln Val
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<210> 50
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Val Thr Ile Thr Ile Thr Gln Gly Gly Gly Gly Ser
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<210> 52

<211> 14

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<223> FcgammaRIIIA-G2, V3 subsequence

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<223> FcgammaRIIIA-G2, V4 subsequence

<400> 53

Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Glu
1 5 10

<210> 54

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<223> FcgammaRIIB-G2 wild type subsequence

<400> 54

Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Glu
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